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<110> Arkowitz, Robert A
Nern, Peter MA

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<151> 2000-04-07

<150> US 09/732,180
<151> 2000-12-07

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<151> 1998-06-12

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<220>
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Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 3
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<220>
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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
cagctggtca aagtgctaga agtagtagaa acgctaatga attccagc 228

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<211> 76
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: amino acid

<400> 4
Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15

Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 5
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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: amino acid

<400> 6
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1 5 10 15

Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 7
<211> 228
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleic acid

<400> 7
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gacgatttga aagtctgtaa aaaatccatt tatgacttta tattgggctg caagaaacac 120
tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
cagctggtca aagtgctaga agtagtagaa acgctaatga attccagc 228

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: amino acid

<400> 8
Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro

1 5 10 15

Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 9
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

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Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu
20 25 30

Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
35 40 45

Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
50 55 60

Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
65 70 75 80

His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
85 90 95

Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
100 105 110

Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
115 120 125

Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
130 135 140

Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
145 150 155 160

Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
165 170 175

Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
180 185 190

Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe

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Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg
    210                 215                 220

Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu
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Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser
                245                 250                 255

Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly
            260                 265                 270

Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser
        275                 280                 285

Asn Asn Ile His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser
    290                 295                 300

Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser
305                 310                 315                 320

Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg
                325                 330                 335

Ile Met Ile Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser
            340                 345                 350

Leu Asn Ile Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu
        355                 360                 365

Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln
    370                 375                 380

Gln Leu Ile His Asp Leu Lys Asn
385                 390
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<210> 10
<211> 1269
<212> DNA
<213> Saccharomyces cerevisiae

<220>
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gccagacaag agagtaaaca gcttcatgct caaataaata aagcaaaaca caagatacaa 180
gatgcaagct tattccagat ggccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240
ttaaagccaa atatcgtgtt gaaaggccat aataataaaa tctcagattt tcggtggagt 300
cgagattcaa aacgtatttt gagtgcaagt caagatggct ttatgcttat atgggacagt 360
gcttcaggtt taaaacagaa cgctattcca ttagattctc aatgggttct ttcctgcgct 420
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<210> 11
<211> 422
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<223>

<400> 11

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Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
             20                  25                  30

Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
         35                  40                  45

His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
     50                  55                  60

Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
 65                  70                  75                  80

Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
                 85                  90                  95

Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
            100                 105                 110

Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
        115                 120                 125

Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
    130                 135                 140

Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
145                 150                 155                 160

Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
                165                 170                 175

Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
            180                 185                 190

His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
        195                 200                 205

Pro Lys Ala Lys Arg Val Arg Glu Tyr Ser Asp His Leu Gly Asp Val
    210                 215                 220
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Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
225   230   235   240

Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
                245   250   255

Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
            260   265   270

Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
        275   280   285

Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
    290   295   300

Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
305   310   315   320

Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
                325   330   335

Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val
            340   345   350

Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
        355   360   365

Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
    370   375   380

Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
385   390   395   400

Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
                405   410   415

Trp Ser Pro Gly Tyr Gln
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<210> 12
<211> 1269
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleic acid

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gatgggttag ctgtatgtac aggttcatgg gactcaacca tgaaaatatg gtctccaggt 1260
tatcaatag 1269

<210> 13
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid sequence

<400> 13
Met Ala His Gln Met Asp Ser Ile Thr Tyr Ser Asn Asn Val Thr Gln
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Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
20 25 30

Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
35 40 45

His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
50 55 60

Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
65 70 75 80

Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
85 90 95

Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
100 105 110

Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
115 120 125

Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
130 135 140

Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
145 150 155 160

Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
165 170 175

Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
180 185 190

His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
195 200 205

Pro Lys Ala Lys Arg Val Arg Gly Tyr Ser Asp His Leu Gly Asp Val

210 215 220

Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
225 230 235 240

Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
245 250 255

Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
260 265 270

Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
275 280 285

Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
290 295 300

Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
305 310 315 320

Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
325 330 335

Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val
340 345 350

Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
355 360 365

Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
370 375 380

Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
385 390 395 400

Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
405 410 415

Trp Ser Pro Gly Tyr Gln
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<210> 14
<211> 1269
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleic acid sequence

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tgctatattt ctgacattga atttacagat aacgcacata tattgacagc aagtggggat 600
atgacatgtg ccttgtggga tataccgaaa gcaaagaggg tgagagaata ttctgaccat 660
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<210> 15
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid sequence

<400> 15
Met Ala His Gln Met Asp Ser Ile Thr Tyr Ser Asn Asn Val Thr Gln
1 5 10 15

Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
20 25 30

Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
35 40 45

His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
50 55 60

Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
65 70 75 80

Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
85 90 95

Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
100 105 110

Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
115 120 125

Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
130 135 140

Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
145 150 155 160

Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
165 170 175

Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
180 185 190

His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile

195 200 205

Pro Lys Ala Lys Arg Val Arg Glu Tyr Ser Asp His Leu Gly Asp Val
210 215 220

Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
225 230 235 240

Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
245 250 255

Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
260 265 270

Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
275 280 285

Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
290 295 300

Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
305 310 315 320

Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
325 330 335

Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Ala Val
340 345 350

Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
355 360 365

Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
370 375 380

Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
385 390 395 400

Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
405 410 415

Trp Ser Pro Gly Tyr Gln
420

<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 16
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1 5

<210> 17
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid sequence

<400> 17
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<210> 18
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid sequence

<400> 18
Gln Phe Lys Leu Pro Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 19
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid sequence

<400> 19
Gln Phe Lys Leu Pro Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 20
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid sequence

<400> 20
Gln Phe Lys Leu Pro Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 21

<211> 19
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<223>

<400> 21
Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 22
<211> 19
<212> PRT
<213> Human

<220>
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<400> 22
Gln Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met
1 5 10 15

Lys Thr Ile

<210> 23
<211> 2535
<212> DNA
<213> Candida albicans

<400> 23
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ttcaataaac caagtactcc caaagaccat ttattctatc gatgtgaatc actaaaacga 180
aaactacaaa aaatccctgg catggaacca tttttgaacc aagctttcaa tcaggctgaa 240
caactcagtg aacaacaagc attggctttg gcacaggaaa gaagcaatgg aaatggacat 300
agtaatggca aacgtcatca atcattagac ggtgccatga atagactttc agttggttct 360
gatagtagtt cgatccaagg ttcattgaca cgaatggcca ccaatgcgtc aacgtcatct 420
ttaatcagtg gtatgccaaa caacaacact ttatttacgt ttactgcagg ggttttacca 480
gctaatatta gtgtcgatcc tgctacccat ctttggaaat tgttccaaca aggggccccc 540
ttttgtgttc ttatcaatca tatccttcct gattcccaaa taccagttgt cagttctgat 600
gacttgagaa tttgcaaaaa atcagtatat gacttttaa ttgccgtcaa gacacaattg 660
aattttgatg acgagaatat gttcactata tccaatgttt tctccgacaa tgcccaagat 720
ttaatcaaga ttattgatgt cattaataaa ctacttgctg agtactcaga tgctagtgac 780
ctgggtggtg gcgatgaaga tgtaaatatg gatgttcaaa ttaccgatga aagatcaaaa 840
gttttccgag aaattatcga aacagaaaga aaatatgttc aagacttgga actaatgtgt 900
aaataccgtc aagatctaat tgaagccgaa aatttgtctt cagaacaaat tcacttgtta 960
ttcccaaatt taaatgagat tattgatttt caaagacgat tcctcaatgg gttagaatgt 1020
aacatcaatg tacctattag atatcaaaga attggatcag tatttattca tgcttctttg 1080
ggcccttca atgcttatga accttggact ataggacaat tgacggcgat tgatttgatc 1140
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caatcgtata tattaaagcc gatccaaaga ttgtgtaaat acccacttt gttgaaagag 1260
ttaatcaaaa catcaccaga atattcaaaa caggaccccc atggcagctc gtcatcgaca 1320
tcattcaatg aattattggt ggctaaaact gcaatgaaag aattggcaaa tcaagtcaat 1380
gaggcgcaaa gacgagcaga aaatatcgaa catttggaaa aactaaaaga aagagtaggt 1440
aattggcgtg ggtttaattt ggatgctcaa ggagaactat tattccacgg acaagttggg 1500

gttaaagatg ctgaaaatga aaaggaatac gttgcttatc tttttgaaaa aatcgtattt 1560
tttttcacag aaattgatga taccaaaaaa tctgataaac aggaaaagaa gagcaagttt 1620
tcgacaagaa agagatcaac ttcatcaaat cttagttcat cgactactaa tttgttggaa 1680
tcaataaaca attcccgaaa ggataacaca ttgccattgg aattaaaggg aagagtttat 1740
atatcggaga tttataacat ttccgcacca aacactcctg gctcaactct aatcatctca 1800
tggtcaggta gaaaggaaag cggctcattc actttgagat atcgtagtga agaagccaga 1860
aaccaatggg aaaagtgttt acgtgatttg aagactaatg aaatgaataa acaaattcat 1920
aagaagttac gtgattccga cctgtcattt aatactgatg actctgccat atatgattac 1980
acgggtatta gtacgtcacc agtcaatcaa tcaactcaac aacaatacta tgatcatcgg 2040
ggctctcaca gttcccgcca tcactcatcg tcatccactt tgagtatgat gaagaataat 2100
agagttaaat ctggtgattt gagtagaata tcttcaactt caacaacatt agattctttc 2160
agtaacaact tgaatgggtc accaaatacc actaatccat ctttgatgtc ttcagatgcc 2220
accaaaacaa ttccaacatt tgacgttgca attaaattgc tttacaaatc gacagaattg 2280
tcagagccat tgattgtcaa tgcacaaatt gagtataatg accttttaca gaaaattatc 2340
tcccagatta tcacttcgaa cttggtggca gatgatgtca atattagtcg attgagatat 2400
aaagacgacg aaggagactt tgtgaatttg aattcagatg atgattgggg gttagtgctt 2460
gatatgttaa ccagtgaaga cttttaccaa acatcaagca atgaaaaacg actggtgaca 2520
gtgtgggttt cttga
2535

<210> 24
<211> 844
<212> PRT
<213> Candida albicans

<400> 24
Met Glu His Pro Pro Ala Ala Leu Arg Thr Phe Ser Thr Gln Ser Thr
1 5 10 15

Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg Ile Val Ser
20 25 30

Ser Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr Pro Lys
35 40 45

Asp His Leu Phe Tyr Arg Cys Glu Ser Leu Lys Arg Lys Leu Gln Lys
50 55 60

Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln Ala Glu
65 70 75 80

Gln Leu Ser Glu Gln Gln Ala Leu Ala Leu Ala Gln Glu Arg Ser Asn
85 90 95

Gly Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp Gly Ala
100 105 110

Met Asn Arg Leu Ser Val Gly Ser Asp Ser Ser Ser Ile Gln Gly Ser
115 120 125

Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile Ser Gly
130 135 140

Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val Leu Pro
145 150 155 160

Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu Phe Gln
165 170 175

Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser
180 185 190

Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser
195 200 205

Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp
210 215 220

Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp
225 230 235 240

Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr Ser
245 250 255

Asp Ala Ser Asp Ser Gly Gly Gly Asp Glu Asp Val Asn Met Asp Val
260 265 270

Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile Glu Thr
275 280 285

Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr Arg Gln
290 295 300

Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His Leu Leu
305 310 315 320

Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe Leu Asn
325 330 335

Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg Ile Gly
340 345 350

Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr Glu Pro
355 360 365

Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys Glu Ala
370 375 380

Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe Glu Leu
385 390 395 400

Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr Pro Leu
405 410 415

Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys Gln Asp
420 425 430

Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu Val Ala
435 440 445

Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala Gln Arg
450 455 460

Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg Val Gly
465 470 475 480

Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu Phe His
485 490 495

Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr Val Ala
500 505 510

Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp Asp Thr
515 520 525

Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr Arg Lys
530 535 540

Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu Leu Glu
545 550 555 560

Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu Leu Lys
565 570 575

Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro Asn Thr
580 585 590

Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu Ser Gly
595 600 605

Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln Trp Glu
610 615 620

Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln Ile His
625 630 635 640

Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp Ser Ala
645 650 655

Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln Ser Thr
660 665 670

Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg His His
675 680 685

Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val Lys Ser
690 695 700

Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp Ser Phe
705 710 715 720

Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser Leu Met
725 730 735

Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala Ile Lys
740 745 750

Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val Asn Ala
755 760 765

Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln Ile Ile
770 775 780

Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu Arg Tyr
785 790 795 800

Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp Asp Trp
805 810 815

Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp Phe Tyr Gln Thr Ser
820 825 830

Ser Asn Glu Lys Arg Ser Val Thr Val Trp Val Ser

<210> 25
<211> 22
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25
Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser
1 5 10 15

Ile Tyr Asp Phe Ile Leu
20

<210> 26
<211> 22
<212> PRT
<213> Candida albicans

<400> 26
Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser
1 5 10 15

Val Tyr Asp Phe Leu Ile
20

<210> 27
<211> 854
<212> PRT
<213> Saccharomyces cerevisiae

<400> 27
Met Ala Ile Gln Thr Arg Phe Ala Ser Gly Thr Ser Leu Ser Asp Leu
1 5 10 15

Lys Pro Lys Pro Ser Ala Thr Ser Ile Ser Ile Pro Met Gln Asn Val
20 25 30

Met Asn Lys Pro Val Thr Glu Gln Asp Ser Leu Phe His Ile Cys Ala
35 40 45

Asn Ile Arg Lys Arg Leu Glu Val Leu Pro Gln Leu Lys Pro Phe Leu
50 55 60

Gln Leu Ala Tyr Gln Ser Ser Glu Val Leu Ser Glu Arg Gln Ser Leu
65 70 75 80

Leu Leu Ser Gln Lys Gln His Gln Glu Leu Leu Lys Ser Asn Gly Ala
85 90 95

Asn Arg Asp Ser Ser Asp Leu Ala Pro Thr Leu Arg Ser Ser Ser Ile
100 105 110

Ser Thr Ala Thr Ser Leu Met Ser Met Glu Gly Ile Ser Tyr Thr Asn
115 120 125

Ser Asn Pro Ser Ala Thr Pro Asn Met Glu Asp Thr Leu Leu Thr Phe
130 135 140

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Ser Met Gly Ile Leu Pro Ile Thr Met Asp Cys Asp Pro Val Thr Gln
145                 150                 155                 160

Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu Cys Ile Leu Phe Asn
                165                 170                 175

Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu
            180                 185                 190

Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile Leu Gly Cys Lys Lys
        195                 200                 205

His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr Ile Ser Asp Val Phe
    210                 215                 220

Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu Glu Val Val Glu Thr
225                 230                 235                 240

Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser Lys Ser Lys Thr Gln
                245                 250                 255

Gln Ile Met Asn Ala Glu Asn Gln His Arg His Gln Pro Gln Gln Ser
            260                 265                 270

Ser Lys Lys His Asn Glu Tyr Val Lys Ile Ile Lys Glu Phe Val Ala
        275                 280                 285

Thr Glu Arg Lys Tyr Val His Asp Leu Glu Ile Leu Asp Lys Tyr Arg
    290                 295                 300

Gln Gln Leu Leu Asp Ser Asn Leu Ile Thr Ser Glu Glu Leu Tyr Met
305                 310                 315                 320

Leu Phe Pro Asn Leu Gly Asp Ala Ile Asp Phe Gln Arg Arg Phe Leu
                325                 330                 335

Ile Ser Leu Glu Ile Asn Ala Leu Val Glu Pro Ser Lys Gln Arg Ile
            340                 345                 350

Gly Ala Leu Phe Met His Ser Lys His Phe Phe Lys Leu Tyr Glu Pro
        355                 360                 365

Trp Ser Ile Gly Gln Asn Ala Ala Ile Glu Phe Leu Ser Ser Thr Leu
    370                 375                 380

His Lys Met Arg Val Asp Glu Ser Gln Arg Phe Ile Ile Asn Asn Lys
385                 390                 395                 400

Leu Glu Leu Gln Ser Phe Leu Tyr Lys Pro Val Gln Arg Leu Cys Arg
                405                 410                 415

Tyr Pro Leu Leu Val Lys Glu Leu Leu Ala Glu Ser Ser Asp Asp Asn
            420                 425                 430

Asn Thr Lys Glu Leu Glu Ala Ala Leu Asp Ile Ser Lys Asn Ile Ala
        435                 440                 445

Arg Ser Ile Asn Glu Asn Gln Arg Arg Thr Glu Asn His Gln Val Val
    450                 455                 460
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Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys Gly Tyr Arg Ile Ser
465 470 475 480

Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val Phe Ile Ser Thr Thr
485 490 495

Asn Ser Ser Ser Glu Pro Glu Arg Glu Phe Glu Val Tyr Leu Phe Glu
500 505 510

Lys Ile Ile Ile Leu Phe Ser Glu Val Val Thr Lys Lys Ser Ala Ser
515 520 525

Ser Leu Ile Leu Lys Lys Lys Ser Ser Thr Ser Ala Ser Ile Ser Ala
530 535 540

Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His His Ser Tyr His Lys
545 550 555 560

Arg His Ser Asn Ser Ser Ser Ser Asn Asn Ile His Leu Ser Ser Ser
565 570 575

Ser Ala Ala Ala Ile Ile His Ser Ser Thr Asn Ser Ser Asp Asn Asn
580 585 590

Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys Leu Ser Ala Asn Glu
595 600 605

Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile Met Asn Leu Asn Gln
610 615 620

Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile Thr Trp Glu Ser Ile
625 630 635 640

Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys Asn Glu Glu Thr Arg
645 650 655

Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile His Asp Leu Lys Asn
660 665 670

Glu Gln Phe Lys Ala Arg His His Ser Ser Thr Ser Thr Thr Ser Ser
675 680 685

Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr Thr Thr Met Asn Thr
690 695 700

Pro Asn His His Asn Ser Arg Gln Thr His Asp Ser Met Ala Ser Phe
705 710 715 720

Ser Ser Ser His Met Lys Arg Val Ser Asp Val Leu Pro Lys Arg Arg
725 730 735

Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys Ser Ile Ser Glu Asn
740 745 750

Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu Phe Arg Ile Ser Tyr
755 760 765

Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu Ile Phe Thr Leu Leu
770 775 780

Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile Met Ala Ile Asn Ser

785 790 795 800

Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser Pro Ile Thr Lys Ile
805 810 815

Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val Leu Gly Ser Asp Glu
820 825 830

Asp Trp Asn Val Ala Lys Glu Met Leu Ala Glu Asn Asn Glu Lys Phe
835 840 845

Leu Asn Ile Arg Leu Tyr
850

<210> 28
<211> 837
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28
Ser Gly Thr Ser Leu Ser Asp Leu Lys Pro Lys Pro Ser Ala Thr Ser
1 5 10 15

Ile Ser Ile Pro Met Gln Asn Val Met Asn Lys Pro Val Thr Glu Gln
20 25 30

Asp Ser Leu Phe His Ile Cys Ala Asn Ile Arg Lys Arg Leu Glu Val
35 40 45

Leu Pro Gln Leu Lys Pro Phe Leu Gln Leu Ala Tyr Gln Ser Ser Glu
50 55 60

Val Leu Ser Glu Arg Gln Ser Leu Leu Leu Ser Gln Lys Gln His Gln
65 70 75 80

Glu Leu Leu Lys Ser Asn Gly Ala Asn Arg Asp Ser Ser Asp Leu Ala
85 90 95

Pro Thr Leu Arg Ser Ser Ser Ile Ser Thr Ala Thr Ser Leu Met Ser
100 105 110

Met Glu Gly Ile Ser Tyr Thr Asn Ser Asn Pro Ser Ala Thr Pro Asn
115 120 125

Met Glu Asp Thr Leu Leu Thr Phe Ser Met Gly Ile Leu Pro Ile Thr
130 135 140

Met Asp Cys Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gln Gly
145 150 155 160

Ala Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu
165 170 175

Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr
180 185 190

Asp Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu
195 200 205

Leu Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val

210 215 220

Lys Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile
225 230 235 240

Phe Pro Ser Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln
245 250 255

His Arg His Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val
260 265 270

Lys Ile Ile Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp
275 280 285

Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu
290 295 300

Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
305 310 315 320

Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
325 330 335

Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
340 345 350

His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
355 360 365

Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
370 375 380

Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
385 390 395 400

Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
405 410 415

Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
420 425 430

Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
435 440 445

Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
450 455 460

Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe
465 470 475 480

Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg
485 490 495

Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu
500 505 510

Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser
515 520 525

Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly
530 535 540

Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser
545 550 555 560

Asn Asn Ile His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser
565 570 575

Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser
580 585 590

Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg
595 600 605

Ile Met Ile Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser
610 615 620

Leu Asn Ile Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu
625 630 635 640

Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln
645 650 655

Gln Leu Ile His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His
660 665 670

Ser Ser Thr Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met
675 680 685

Ser Pro Thr Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln
690 695 700

Thr His Asp Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val
705 710 715 720

Ser Asp Val Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser
725 730 735

Glu Ile Lys Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser
740 745 750

Ser Ile Leu Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser
755 760 765

Ser Ser Glu Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp
770 775 780

Asp Leu Ile Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn
785 790 795 800

Asn Ile Ser Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp
805 810 815

Phe Val Val Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu Met
820 825 830

Leu Ala Glu Asn Asn
835

<210> 29
<211> 813

<212> PRT
<213> Candida albicans

<400> 29

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Ser Thr Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg Ile
  1               5                  10                  15

Val Ser Ser Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr
             20                  25                  30

Pro Lys Asp His Leu Phe Tyr Arg Cys Glu Ser Leu Lys Arg Lys Leu
         35                  40                  45

Gln Lys Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln
     50                  55                  60

Ala Glu Gln Leu Ser Glu Gln Gln Ala Leu Ala Leu Ala Gln Glu Arg
 65                  70                  75                  80

Ser Asn Gly Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp
                 85                  90                  95

Gly Ala Met Asn Arg Leu Ser Val Gly Ser Asp Ser Ser Ser Ile Gln
            100                 105                 110

Gly Ser Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile
        115                 120                 125

Ser Gly Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val
    130                 135                 140

Leu Pro Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu
145                 150                 155                 160

Phe Gln Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro
                165                 170                 175

Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
            180                 185                 190

Lys Ser Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe
        195                 200                 205

Asp Asp Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala
    210                 215                 220

Gln Asp Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu
225                 230                 235                 240

Tyr Ser Asp Ala Ser Asp Ser Gly Gly Gly Asp Glu Asp Val Asn Met
                245                 250                 255

Asp Val Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile
            260                 265                 270

Glu Thr Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr
        275                 280                 285

Arg Gln Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His
    290                 295                 300
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Leu Leu Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe
305 310 315 320

Leu Asn Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg
325 330 335

Ile Gly Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr
340 345 350

Glu Pro Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys
355 360 365

Glu Ala Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe
370 375 380

Glu Leu Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr
385 390 395 400

Pro Leu Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys
405 410 415

Gln Asp Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu
420 425 430

Val Ala Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala
435 440 445

Gln Arg Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg
450 455 460

Val Gly Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu
465 470 475 480

Phe His Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr
485 490 495

Val Ala Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp
500 505 510

Asp Thr Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr
515 520 525

Arg Lys Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu
530 535 540

Leu Glu Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu
545 550 555 560

Leu Lys Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro
565 570 575

Asn Thr Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu
580 585 590

Ser Gly Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln
595 600 605

Trp Glu Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln
610 615 620

Ile His Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp

625 630 635 640

Ser Ala Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln
645 650 655

Ser Thr Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg
660 665 670

His His Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val
675 680 685

Lys Ser Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp
690 695 700

Ser Phe Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser
705 710 715 720

Leu Met Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala
725 730 735

Ile Lys Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val
740 745 750

Asn Ala Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln
755 760 765

Ile Ile Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu
770 775 780

Arg Tyr Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp
785 790 795 800

Asp Trp Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp
805 810

<210> 30
<211> 684
<212> PRT
<213> Saccharomyces cerevisiae

<400> 30
Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu
1 5 10 15

Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile
20 25 30

Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile
35 40 45

Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr
50 55 60

Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu
65 70 75 80

Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser
85 90 95

Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln His Arg His

100 105 110

Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val Lys Ile Ile
115 120 125

Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp Leu Glu Ile
130 135 140

Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu Ile Thr Ser
145 150 155 160

Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala Ile Asp Phe
165 170 175

Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu Val Glu Pro
180 185 190

Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys His Phe Phe
195 200 205

Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala Ile Glu Phe
210 215 220

Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser Gln Arg Phe
225 230 235 240

Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr Lys Pro Val
245 250 255

Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu Leu Ala Glu
260 265 270

Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala Leu Asp Ile
275 280 285

Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg Arg Thr Glu
290 295 300

Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys
305 310 315 320

Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val
325 330 335

Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg Glu Phe Glu
340 345 350

Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu Val Val Thr
355 360 365

Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser Ser Thr Ser
370 375 380

Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His
385 390 395 400

His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser Asn Asn Ile
405 410 415

His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser Ser Thr Asn
420 425 430

Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys
435 440 445

Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile
450 455 460

Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile
465 470 475 480

Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys
485 490 495

Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile
500 505 510

His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His Ser Ser Thr
515 520 525

Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr
530 535 540

Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln Thr His Asp
545 550 555 560

Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val Ser Asp Val
565 570 575

Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys
580 585 590

Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu
595 600 605

Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu
610 615 620

Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile
625 630 635 640

Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser
645 650 655

Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val
660 665 670

Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu
675 680

<210> 31
<211> 742
<212> PRT
<213> Schizosaccharomyces pombe

<400> 31
Asp Pro Val Thr Glu Ile Trp Leu Phe Cys Arg Leu Gly Tyr Pro Leu
1 5 10 15

Cys Ala Leu Phe Asn Cys Leu Pro Val Lys Gln Lys Leu Glu Val Asn
20 25 30

Ser Ser Val Ser Leu Glu Asn Thr Asn Val Cys Lys Ala Ser Leu Tyr
35 40 45

Arg Phe Met Leu Met Cys Lys Asn Glu Leu Gly Leu Thr Asp Ala Ala
50 55 60

Leu Phe Ser Ile Ser Glu Ile Tyr Lys Pro Ser Thr Ala Pro Leu Val
65 70 75 80

Arg Ala Leu Gln Thr Ile Glu Leu Leu Leu Lys Lys Tyr Glu Val Ser
85 90 95

Asn Thr Thr Lys Ser Ser Ser Thr Pro Ser Pro Ser Thr Asp Asp Asn
100 105 110

Val Pro Thr Gly Thr Leu Asn Ser Leu Ile Ala Ser Gly Arg Arg Val
115 120 125

Thr Ala Glu Leu Tyr Glu Thr Glu Leu Lys Tyr Ile Gln Asp Leu Glu
130 135 140

Tyr Leu Ser Asn Tyr Met Val Ile Leu Gln Gln Lys Gln Ile Leu Ser
145 150 155 160

Gln Asp Thr Ile Leu Ser Ile Phe Thr Asn Leu Asn Glu Ile Leu Asp
165 170 175

Phe Gln Arg Arg Phe Leu Val Gly Leu Glu Met Asn Leu Ser Leu Pro
180 185 190

Val Glu Glu Gln Arg Leu Gly Ala Leu Phe Ile Ala Leu Glu Glu Gly
195 200 205

Phe Ser Val Tyr Gln Val Phe Cys Thr Asn Phe Pro Asn Ala Gln Gln
210 215 220

Leu Ile Ile Asp Asn Gln Asn Gln Leu Leu Lys Val Ala Asn Leu Leu
225 230 235 240

Glu Pro Ser Tyr Glu Leu Pro Ala Leu Leu Ile Lys Pro Ile Gln Arg
245 250 255

Ile Cys Lys Tyr Pro Leu Leu Leu Asn Gln Leu Leu Lys Gly Thr Pro
260 265 270

Ser Gly Tyr Gln Tyr Glu Glu Glu Leu Lys Gln Gly Met Ala Cys Val
275 280 285

Val Arg Val Ala Asn Gln Val Asn Glu Thr Arg Arg Ile His Glu Asn
290 295 300

Arg Asn Ala Ile Ile Glu Leu Glu Gln Arg Val Ile Asp Trp Lys Gly
305 310 315 320

Tyr Ser Leu Gln Tyr Phe Gly Gln Leu Leu Val Trp Asp Val Val Asn
325 330 335

Val Cys Lys Ala Asp Ile Glu Arg Glu Tyr His Val Tyr Leu Phe Glu
340 345 350

Lys Ile Leu Leu Cys Cys Lys Glu Met Ser Thr Leu Lys Arg Gln Ala
355 360 365

Arg Ser Ile Ser Met Asn Lys Lys Thr Lys Arg Leu Asp Ser Leu Gln
370 375 380

Leu Lys Gly Arg Ile Leu Thr Ser Asn Ile Thr Thr Val Val Pro Asn
385 390 395 400

His His Met Gly Ser Tyr Ala Ile Gln Ile Phe Trp Arg Gly Asp Pro
405 410 415

Gln His Glu Ser Phe Ile Leu Lys Leu Arg Asn Glu Glu Ser His Lys
420 425 430

Leu Trp Met Ser Val Leu Asn Arg Leu Leu Trp Lys Asn Glu His Gly
435 440 445

Ser Pro Lys Asp Ile Arg Ser Ala Ala Ser Thr Pro Ala Asn Pro Val
450 455 460

Tyr Asn Arg Ser Ser Ser Gln Thr Ser Lys Gly Tyr Asn Ser Ser Asp
465 470 475 480

Tyr Asp Leu Leu Arg Thr His Ser Leu Asp Glu Asn Val Asn Ser Pro
485 490 495

Thr Ser Ile Ser Ser Pro Ser Ser Lys Ser Ser Pro Phe Thr Lys Thr
500 505 510

Thr Ser Lys Asp Thr Lys Ser Ala Thr Thr Thr Asp Glu Arg Pro Ser
515 520 525

Asp Phe Ile Arg Leu Asn Ser Glu Glu Ser Val Gly Thr Ser Ser Leu
530 535 540

Arg Thr Ser Gln Thr Thr Ser Thr Ile Val Ser Asn Asp Ser Ser Ser
545 550 555 560

Thr Ala Ser Ile Pro Ser Gln Ile Ser Arg Ile Ser Gln Val Asn Ser
565 570 575

Leu Leu Asn Asp Tyr Asn Tyr Asn Arg Gln Ser His Ile Thr Arg Val
580 585 590

Tyr Ser Gly Thr Asp Asp Gly Ser Ser Val Ser Ile Phe Glu Asp Thr
595 600 605

Ser Ser Ser Thr Lys Gln Lys Ile Phe Asp Gln Pro Thr Thr Asn Asp
610 615 620

Cys Asp Val Met Arg Pro Arg Gln Tyr Ser Tyr Ser Ala Gly Met Lys
625 630 635 640

Ser Asp Gly Ser Leu Leu Pro Ser Thr Lys His Thr Ser Leu Ser Ser
645 650 655

Ser Ser Thr Ser Thr Ser Leu Ser Val Arg Asn Thr Thr Asn Val Lys
660 665 670

Ile Arg Leu Arg Leu His Glu Val Ser Leu Val Leu Val Val Ala His

675 680 685

Asp Ile Thr Phe Asp Glu Leu Leu Ala Lys Val Glu His Lys Ile Lys
690 695 700

Leu Cys Gly Ile Leu Lys Gln Ala Val Pro Phe Arg Val Arg Leu Lys
705 710 715 720

Tyr Val Asp Glu Asp Gly Asp Phe Ile Thr Ile Thr Ser Asp Glu Asp
725 730 735

Val Leu Met Ala Phe Glu
740

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> misc_feature
<222> (12)
<223> n is a or c or g or t

<400> 32
aartayrtkc angayttrga 20

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> misc_feature
<222> (13)
<223> n is a or c or g or t

<400> 33
rattttytcr aanarrta 18

<210> 34
<211> 76
<212> PRT
<213> Candida albicans

<400> 34
Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
1 5 10 15

Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
20 25 30

Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met

35 40 45

Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
50 55 60

Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr
65 70 75

<210> 35 <211> 19 <212> PRT <213> Candida albicans <400> 35

Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
1 5 10 15

Lys Ser Val

<210> 36
<211> 73
<212> PRT
<213> Candida albicans

<400> 36
Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
1 5 10 15

Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
20 25 30

Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met
35 40 45

Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
50 55 60

Ile Ile Asp Val Ile Asn Lys Leu Leu
65 70

<210> 37
<211> 73
<212> PRT
<213> Saccharomyces cerevisiae

<400> 37
Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15

Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met
65 70